In the Specification

The following paragraph numbers refer to the paragraphs as numbered in the application as published (US Application Publication No. 20040110219).

Please replace paragraph [0033] with the following rewritten paragraph.

--[0033] FIG. 3 Relative expression (~~Taqman©~~ TAQMAN® quantitative PCR) (Roche) of mRNA in samples derived from adenocarcinomas of the pancreas (PaCa), chronic pancreatitis (ChronPa) and normal pancreatic tissues (N or PA).--

Please replace paragraph [0040] with the following rewritten paragraph.

--[0040] UKW polypeptides can be identified in diagnostic assays using specific probes and primers. Usually such methods include amplifying the target sequence in the sample by amplification methods such as the PCR method. Quantitative detection can be performed by PCR techniques, preferably by the use of quantitative RT-PCR using, e.g., the ~~LightCycler®~~ LIGHTCYCLER® of Roche Diagnostics GmbH, DE.--

Please replace paragraph [0041] with the following rewritten paragraph.

--[0041] In a preferred embodiment of the invention the coding nucleic acid of the sample is amplified before the test, for example by means of the known PCR technique. Usually a derivatized (labeled) nucleic acid probe is used within the framework of nucleic acid diagnostics. This probe is contacted with a denatured DNA, RNA or RT-DNA from the sample which is bound to a carrier and in this process the temperature, ionic strength, pH and other buffer conditions are selected--depending on the length and composition of the nucleic acid probe and the resulting melting temperature of the expected hybrid--such that the labeled DNA or RNA can bind to homologous DNA or RNA (hybridization see also Wahl, G. M., et al., Proc. Natl. Acad. Sci. USA 76 (1979)

3683-3687). Suitable carriers are membranes or carrier materials based on nitrocellulose (e.g., Schleicher and Schull, BA 85, AMERSHAM HYBOND® C ~~Amersham Hybond, C.~~), strengthened or bound nitrocellulose in powder form or nylon membranes derivatized with various functional groups (e.g.; nitro groups) (e.g., ~~Schleicher and Schull, Nytran~~ NYTRAN®; ~~NEN, Gene Screen~~ GENESCREEN®; AMERSHAM HYBOND® M ~~Amersham Hybond M.~~; ~~Pall Biodyne~~ PALL BIODYNE®).--

Please replace paragraph [0066] with the following rewritten paragraph.

--[0066] Antibodies which are useful according to the invention, especially for therapeutic purposes, can be identified by reducing the proliferation and invasive potential of pancreatic tumor cells. For this purpose, pancreatic tumor cells or a pancreatic tumor cell line, preferably cell line SUIT-2 607 are treated with an antibody against UKW and proliferation and invasive potential are measured by Cell Proliferation Reagent WST-1 (a tetrazolium salt reagent, Roche Diagnostics GmbH, DE) and MATRIGEL™ ~~Matrigel~~ invasion assay (BDS Biosciences, www.bdbiosciences.com).--

Please replace paragraph [0068] with the following rewritten paragraph.

--[0068] Monoclonal antibodies can be isolated and purified from hybridoma cultures by a variety of well-established techniques. Such isolation techniques include affinity chromatography with PROTEIN-A SEPHAROSE® ~~Protein-A Sepharose~~, size-exclusion chromatography, and ion-exchange chromatography (see, for example, Coligan at pages 2.7.1-2.7.12 and pages 2.9.1-2.9.3; Baines et al., "Purification of Immunoglobulin G (IgG)", In: Methods in Molecular Biology, Vol. 10, pages 79-104, The Humana Press, Inc., 1992).--

Please replace paragraph [0077] with the following rewritten paragraph.

--[0077] 10 μg of total RNA from SUIT-2 007 and SUIT-2 028 cell lines were loaded side by side on a denaturing 1% agarose formaldehyde gel and size-separated by electrophoresis. Blotting to BRIGHTSTAR-PLUS ~~BrightStar-Plus~~™ positively charged nylon membrane was performed by capillary downward transfer. After UV-crosslinking (STRATAGENE UV STRATALINKER® 2400 ~~Stratagene UV Stratalinker 2400~~) the blot was hybridized. The RT-PCR product was labeled with α-[^{32}P]dATP to a specific activity of 2x10^9 cpm/μg using the STRIP-EZ ~~Strip-EZ~~™ DNA Kit (Ambion Inc., Austin, Tex.). Pre-hybridization (30 min) and hybridization (over-night) with the radioactive probe was performed in EXPRESSHYB ~~ExpressHyb~~™ Hybridization Solution (Clontech, Palo Alto, Calif., USA) at 68°C. The membrane was washed in solution 1 (2xSSC, 0.05% SDS) at room temperature for 30-40 min with continuous agitation and several replacements of the wash solution 1 followed by a washing step with solution 2 (0.1xSSC, 0.1% SDS) at 50°C for 40 min with one change of fresh solution. The membrane was then exposed to CRONEX® ~~Cronex~~, Medical X-Ray Films (Sterling Diagnostic Imaging Inc., USA) at -70°C for 2 h. Equal loading and transfer of mRNA to the membrane was assessed by rehybridizing the blot with α-[^{32}P]dATP-labeled GAPDH cDNA probe.—

Please replace paragraph [0080] with the following re-written paragraph.

--[0080] TAQMAN ~~Taqman~~®-PCR--

Please replace paragraph [0081] with the following re-written paragraph.

--[0081] Real-time quantitative PCRs were performed with the TAQMAN ~~TaqMan~~® technology and the ABI PRISM® 7700 apparatus (Applied Biosystems, Foster City, Calif.). 10 μg total RNA isolated from frozen adenocarcinomas of the pancreas, chronic pancreatitis and normal pancreatic tissues were used for reverse transcriptase reactions in a volume of 20 μl. The PCRs were then carried out by mixing 200 ng cDNA with 4 μl of 10xSYBR®- Green buffer, 3 mM $MgCl_2$, 1 mM dNTDs, 0.2 units Uracil-N Glycosylase, 1 unit AMPLITAQ® ~~AmpliTaq~~ Gold, 4 μl primer mix (300 nM each primer: forward

5'TTCTCTTTGACAGGTTCTGGGC3' (SEQ ID NO:3); reverse 5'GGTTGGAACCAGTAGGGCCTC3') (SEQ ID NO:4) in a final volume of 40 µl. PCR primers were designed to generate a DNA fragment of 50 bp using the PRIMER EXPRESS® ~~Primer Express~~ Software (PE Biosystems, CA, USA). The amplification cycles were as follows: 2 min at 50°C followed by 10 min at 95°C and 40 amplification cycles (95°C for 15 sec and 60°C for 60 sec). These experiments were performed twice. The results were calculated by subtraction of gene UKW and housekeeping gene RNA steady-state levels for each sample. Each value was divided by the averaged steady-state level of UKW mRNA of three healthy tissues. Ratios were squared and a reciprocal value was formed.--

Please replace paragraph [0083] with the following re-written paragraph.

--[0083] ~~LightCycler~~ LIGHTCYCLER®-PCR--

Please replace paragraph [0084] with the following re-written paragraph.

--[0084] ~~LightCycler~~ LIGHTCYCLER® quantitative PCR was performed with a ~~LightCycler~~ LIGHTCYCLER® (Roche Molecular Biochemicals, Mannheim, Germany) in ~~LightCycler~~ LIGHTCYCLER® capillaries using a commercially available master mix containing Taq DNA polymerase, SYBR®-Green I, deoxyribonucleoside triphosphates (~~LightCycler~~ LIGHTCYCLER® DNA master SYBR®-Green I, Roche Molecular Biochemicals). After addition of primers (forward 5'CCCCAGGAGTTTATGCTTGG3' (SEQ ID NO:7); reverse 5'GCCTGGATACCACACTACCAG3' (SEQ ID NO:8); final concentration: 0.5 µM), $MgCl_2$ (3 mM) and template DNA to the master mix, 37 cycles of denaturation (95°C for 1 sec), annealing (58°C for 5 sec) and extension (72°C for 8 sec) were performed. All temperature transition rates were set to 20°C per sec. After completion of PCR amplification, melting curve analysis was performed. For this procedure, PCR products were denatured at 95°C, annealed at 65°C, and gradually heated to 95°C SYBR®-Green I fluorescence was monitored stepwise every 0.1°C. The

melting curve was analyzed by visual inspection, amplified UKW gene rearranged structures were melting at 85-88°C. To control for primer dimer formation a control without template DNA (`water control`) was included in each experiment. A small peak was usually visible at 78°C, which could be differentiated from the peak caused by the specific amplification product at 85-88°C. Calibration curve for calnexin was generated using serial dilutions (1:10, 1:50 and 1:80) of cDNA from pancreatic cancer cell line Suit-2 007. The relative amounts of UKW cDNA and calnexin were determined based on a calibration curve. Relative expression of gene UKW was calculated as a normalized value generated by dividing the steady-state levels of gene UKW and calnexin for each sample. Calnexin forward primer 5'ATTGTCAGATCGTTCATTGC3' (SEQ ID NO:9); reverse primer 5'ATGGAACAGGTAACCAGCAT3' (SEQ ID NO:10).--